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CLAIMS

1. Method for the detection and identification of at least one micro-organism, or for the simultaneous detection of several micro-organisms in a sample, comprising the steps of:

(i) if need be releasing, isolating and/or concentrating the polynucleic acids from the micro-organism(s) to be detected in the sample;

(ii) if need be amplifying the 16S-23S rRNA spacer region, or a part of it, from the micro-organism(s) to be detected, with at least one suitable primer pair;

(iii) hybridizing the polynucleic acids of step (i) or (ii) with a set of probes comprising at least two probes under the same hybridization and wash conditions, with said probes being selected from the sequences of table 1a or equivalents thereof, and/or from taxon-specific probes derived from any of the spacer sequences as represented in figures 1-103, with said taxon-specific probe being selected such that it is capable of hybridizing under the same hybridization and wash conditions as at least one of the probes of table 1a ;

(iv) detecting the hybrids formed in step (iii);

(v) identification of the micro-organism(s) present in the sample from the differential hybridization signals obtained in step (iv).

2. Method according to claim 1, wherein said sample is originating from the respiratory tract and wherein wherein the set of probes as defined in step (iii) comprises at least one probe chosen from the following spacer probes:

MYC-ICG-1 :	ACTGGATAGTGGTTGCGAGCATCTA	(SEQ ID NO 1)
MYC-ICG-22 :	CTTCTGAATAGTGGTTGCGAGCATCT	(SEQ ID NO 2)
MTB-ICG-1 :	GGGTGCATGACAACAAAGTTGGCCA	(SEQ ID NO 3)
MTB-ICG-2 :	GACTTGTTCCAGGTGTTGTCCCAC	(SEQ ID NO 4)
MTB-ICG-3 :	CGGCTAGCGGTGGCGTGTTCT	(SEQ ID NO 5)
MAI-ICG-1 :	CAACAGCAAATGATTGCCAGACACAC	(SEQ ID NO 6)
MIL-ICG-11 :	GAGGGGTTCCCGTCTGTAGTG	(SEQ ID NO 7)
MIL-ICG-22 :	TGAGGGGTTCTCGTCTGTAGTG	(SEQ ID NO 8)
MAC-ICG-1 :	CACTCGGTCGATCCGTGTGGA	(SEQ ID NO 9)
MAV-ICG-1 :	TCGGTCCGTCCGTGTGGAGTC	(SEQ ID NO 10)

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MAV-ICG-22 :	GTGGCCGGCGTTCATCGAAA	(SEQ ID NO 11)
MIN-ICG-1 :	GCATAGTCCTTAGGGCTGATGCGTT	(SEQ ID NO 12)
MIN-ICG-2 :	GCTGATGCGTTCGTCGAAATGTGTA	(SEQ ID NO 13)
MIN-ICG-22 :	CTGATGCGTTCGTCGAAATGTGT	(SEQ ID NO 14)
MIN-ICG-222 :	TGATGCGTTCGTCGAAATGTGT	(SEQ ID NO 15)
MIN-ICG-2222 :	GGCTGATGCGTTCGTCGAAATGTGTAA	(SEQ ID NO 16)
MAL-ICG-1 :	ACTAGATGAACGCGTAGTCCTTGT	(SEQ ID NO 17)
MHEF-ICG-1 :	TGGACGAAAACCGGGTGCACAA	(SEQ ID NO 18)
MAH-ICG-1 :	GTGTAATTTCTTTTTTAACTCTTGTGTGTAAGTAAGTG	(SEQ ID NO 19)
MCO-ICG-11 :	TGGCCGGCGTGTTCATCGAAA	(SEQ ID NO 20)
MTH-ICG-11 :	GCACTTCAATTGGTGAAGTGCGAGCC	(SEQ ID NO 21)
MTH-ICG-2 :	GCGTGGTCTTCATGGCCGG	(SEQ ID NO 22)
MEF-ICG-11 :	ACGCGTGGTCCTTCGTGG	(SEQ ID NO 23)
MSC-ICG-1 :	TCGGCTCGTTCTGAGTGGTGTC	(SEQ ID NO 24)
MKA-ICG-1 :	GATGCGTTTGCTACGGGTAGCGT	(SEQ ID NO 25)
MKA-ICG-2 :	GATGCGTTGCCTACGGGTAGCGT	(SEQ ID NO 26)
MKA-ICG-3 :	ATGCGTTGCCCTACGGGTAGCGT	(SEQ ID NO 27)
MKA-ICG-4 :	CGGGCTCTGTTCGAGAGTTGTC	(SEQ ID NO 28)
MKA-ICG-5 :	CCCTCAGGGATTTTCTGGGTGTTG	(SEQ ID NO 182)
MKA-ICG-6 :	GGACTCGTCCAAGAGTGTTGTCC	(SEQ ID NO 183)
MKA-ICG-7 :	TCGGGCTTGGCCAGAGCTGTT	(SEQ ID NO 184)
MKA-ICG-8 :	GGGTGCGCAACAGCAAGCGA	(SEQ ID NO 185)
MKA-ICG-9 :	GATGCGTTGCCCCTACGGG	(SEQ ID NO 186)
MKA-ICG-10 :	CCCTACGGGTAGCGTGTTCTTTTG	(SEQ ID NO 187)
MCH-ICG-1 :	GGTGTGGACTTTGACTTCTGAATAG	(SEQ ID NO 29)
MCH-ICG-2 :	CGGCAAAACGTCGGACTGTCA	(SEQ ID NO 30)
MCH-ICG-3 :	GGTGTGGTCCTTGACTTATGGATAG	(SEQ ID NO 210)
MGO-ICG-1 :	AACACCCTCGGGTGCTGTCC	(SEQ ID NO 31)
MGO-ICG-2 :	GTATGCGTTGTCGTTCGCGGC	(SEQ ID NO 32)
MGO-ICG-5 :	CGTGAGGGGTCATCGTCTGTAG	(SEQ ID NO 33)
MUL-ICG-1 :	GGTTTCGGGATGTTGTCCCACC	(SEQ ID NO 175)

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MGV-ICG-1 : CGACTGAGGTCGACGTGGTGT (SEQ ID NO 176)
MGV-ICG-2 : GGTGTTTGAGCATTGAATAGTGGTTGC (SEQ ID NO 177)
MGV-ICG-3 : TCGGGCCGCGTGTTCGTCAAA (SEQ ID NO 211)
MXE-ICG-1 : GTTGGGCAGCAGGCAGTAACC (SEQ ID NO 178)
MSI-ICG-1 : CCGGCAACGGTTACGTGTTC (SEQ ID NO 179)
MFO-ICG-1 : TCGTTGGATGGCCTCGCACCT (SEQ ID NO 180)
MFO-ICG-2 : ACTTGGCGTGGGATGCGGGAA (SEQ ID NO 181)
MML-ICG-1 : CGGATCGATTGAGTGCTTGTCCC (SEQ ID NO 188)
MML-ICG-2 : TCTAAATGAACGCACTGCCGATGG (SEQ ID NO 189)
MCE-ICG-1 : TGAGGGAGCCCGTGCCTGTA (SEQ ID NO 190)
MHP-ICG-1 : CATGTTGGGCTTGATCGGGTGC (SEQ ID NO 191)
PA-ICG 1 : TGGTGTGCTGCGTGATCCGAT (SEQ ID NO 34)
PA-ICG 2 : TGAATGTTCGTGGATGAACATTGATT (SEQ ID NO 35)
PA-ICG 3 : CACTGGTGATCATTCAAGTCAAG (SEQ ID NO 36)
PA-ICG 4 : TGAATGTTCGT(G/A)(G/A)ATGAACATTGATTTCTGGTC (SEQ ID NO 37)
PA-ICG 5 : CTCTTTCACTGGTGATCATTCAAGTCAAG (SEQ ID NO 38)
MPN-ICG 1 : ATCGGTGGTAAATTAAACCCAAATCCCTGT (SEQ ID NO 49)
MPN-ICG 2 : CAGTTCTGAAAGAACATTTCCGCTTCTTTC (SEQ ID NO 50)
MGE-ICG 1 : CACCCATTAATTTTTTCGGTGTTAAAACCC (SEQ ID NO 51)
Mycoplasma-ICG : CAAAACTGAAAACGACAATCTTTCTAGTTCC (SEQ ID NO 52)
STAU-ICG 1 : TACCAAGCAAAACCGAGTGAATAAAGAGTT (SEQ ID NO 53)
STAU-ICG 2 : CAGAAGATGCGGAATAACGTGAC (SEQ ID NO 54)
STAU-ICG 3 : AACGAAGCCGTATGTGAGCATTTGAC (SEQ ID NO 55)
STAU-ICG 4 : GAACGTAACTTCATGTTAACGTTTGACTTAT (SEQ ID NO 56)
ACI-ICG 1 : GCTTAAGTGCACAGTGCTCTAAACTGA (SEQ ID NO 57)
ACI-ICG 2 : CACGGTAATTAGTGTGATCTGACGAAG (SEQ ID NO 58)

and more preferably from the following spacer probes:

MYC-ICG-1 : ACTGGATAGTGGTTGCGAGCATCTA (SEQ ID NO 1)
MYC-ICG-22 : CTTCTGAATAGTGGTTGCGAGCATCT (SEQ ID NO 2)
MTB-ICG-1 : GGGTGCATGACAACAAAGTTGGCCA (SEQ ID NO 3)
MTB-ICG-2 : GACTTGTTCCAGGTGTTGTCCCAC (SEQ ID NO 4)

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MTB-ICG-3 :	CGGCTAGCGGTGGCGTGTTCT	(SEQ ID NO 5)
MAI-ICG-1 :	CAACAGCAAATGATTGCCAGACACAC	(SEQ ID NO 6)
MIL-ICG-11 :	GAGGGGTTCCCGTCTGTAGTG	(SEQ ID NO 7)
MIL-ICG-22 :	TGAGGGGTTCTCGTCTGTAGTG	(SEQ ID NO 8)
MAC-ICG-1 :	CACTCGGTCGATCCGTGTGGA	(SEQ ID NO 9)
MAV-ICG-1 :	TCGGTCCGTCCGTGTGGAGTC	(SEQ ID NO 10)
MAV-ICG-22 :	GTGGCCGGCGTTCATCGAAA	(SEQ ID NO 11)
MIN-ICG-1 :	GCATAGTCCTTAGGGCTGATGCGTT	(SEQ ID NO 12)
MAL-ICG-1 :	ACTAGATGAACGCGTAGTCCTTGT	(SEQ ID NO 17)
MCO-ICG-11 :	TGGCCGGCGTGTTCATCGAAA	(SEQ ID NO 20)
MTH-ICG-11 :	GCACTTCAATTGGTGAAGTGCGAGCC	(SEQ ID NO 21)
MTH-ICG-2 :	GCGTGGTCTTCATGGCCGG	(SEQ ID NO 22)
MEF-ICG-11 :	ACGCGTGGTCCTTCGTGG	(SEQ ID NO 23)
MSC-ICG-1 :	TCGGCTCGTTCTGAGTGGTGTC	(SEQ ID NO 24)
MKA-ICG-3 :	ATGCGTTGCCCTACGGGTAGCGT	(SEQ ID NO 27)
MKA-ICG-4 :	CGGGCTCTGTTCGAGAGTTGTC	(SEQ ID NO 28)
MKA-ICG-5 :	CCCTCAGGGATTTTCTGGGTGTTG	(SEQ ID NO 182)
MKA-ICG-6 :	GGACTCGTCCAAGAGTGTTGTCC	(SEQ ID NO 183)
MKA-ICG-7 :	TCGGGCTTGGCCAGAGCTGTT	(SEQ ID NO 184)
MKA-ICG-8 :	GGGTGCGCAACAGCAAGCGA	(SEQ ID NO 185)
MKA-ICG-9 :	GATGCGTTGCCCCTACGGG	(SEQ ID NO 186)
MKA-ICG-10 :	CCCTACGGGTAGCGTGTTCTTTTG	(SEQ ID NO 187)
MCH-ICG-1 :	GGTGTGGACTTTGACTTCTGAATAG	(SEQ ID NO 29)
MCH-ICG-2 :	CGGCAAAACGTCGGACTGTCA	(SEQ ID NO 30)
MCH-ICG-3 :	GGTGTGGTCCTTGACTTATGGATAG	(SEQ ID NO 210)
MGO-ICG-5 :	CGTGAGGGGTCATCGTCTGTAG	(SEQ ID NO 33)
MUL-ICG-1 :	GGTTTCGGGATGTTGTCCCACC	(SEQ ID NO 175)
MGV-ICG-1 :	CGACTGAGGTCGACGTGGTGT	(SEQ ID NO 176)
MGV-ICG-2 :	GGTGTTTGAGCATTGAATAGTGGTTGC	(SEQ ID NO 177)
MGV-ICG-3 :	TCGGGCCGCGTGTTCGTCAAA	(SEQ ID NO 211)
MXE-ICG-1 :	GTTGGGCAGCAGGCAGTAACC	(SEQ ID NO 178)
MSI-ICG-1 :	CCGGCAACGGTTACGTGTTC	(SEQ ID NO 179)

MFO-ICG-1 :	TCGTTGGATGGCCTCGCACCT	(SEQ ID NO 180)
MFO-ICG-2 :	ACTTGGCGTGGGATGCGGGAA	(SEQ ID NO 181)
MML-ICG-1 :	CGGATCGATTGAGTGCTTGTCCC	(SEQ ID NO 188)
MML-ICG-2 :	TCTAAATGAACGCACTGCCGATGG	(SEQ ID NO 189)
MCE-ICG-1 :	TGAGGGAGCCCGTGCCTGTA	(SEQ ID NO 190)
MHP-ICG-1 :	CATGTTGGGCTTGATCGGGTGC	(SEQ ID NO 191)
PA-ICG 1 :	TGGTGTGCTGCGTGATCCGAT	(SEQ ID NO 34)
PA-ICG 4 :	TGAATGTTCGT(G/A)(G/A)ATGAACATTGATTTCTGGTC	(SEQ ID NO 37)
PA-ICG 5 :	CTCTTTCACTGGTGATCATTCAAGTCAAG	(SEQ ID NO 38)
MPN-ICG 1 :	ATCGGTGGTAAATTAAACCCAAATCCCTGT	(SEQ ID NO 49)
MPN-ICG 2 :	CAGTTCTGAAAGAACATTTCCGCTTCTTTC	(SEQ ID NO 50)
MGE-ICG 1 :	CACCCATTAATTTTTTCGGTGTTAAAACCC	(SEQ ID NO 51)
Mycoplasma-ICG :	CAAAACTGAAAACGACAATCTTTCTAGTTCC	(SEQ ID NO 52)
STAU-ICG 1 :	TACCAAGCAAAACCGAGTGAATAAAGAGTT	(SEQ ID NO 53)
STAU-ICG 2 :	CAGAAGATGCGGAATAACGTGAC	(SEQ ID NO 54)
STAU-ICG 3 :	AACGAAGCCGTATGTGAGCATTTGAC	(SEQ ID NO 55)
STAU-ICG 4 :	GAACGTAACTTCATGTTAACGTTTGACTTAT	(SEQ ID NO 56)
ACI-ICG 1 :	GCTTAAGTGCACAGTGCTCTAAACTGA	(SEQ ID NO 57)
ACI-ICG 2 :	CACGGTAATTAGTGTGATCTGACGAAG	(SEQ ID NO 58)

or equivalents of said probes,

and/or wherein the set of probes comprises at least one taxon-specific probe derived from the spacer region sequence corresponding to one of the micro-organisms to be detected in said sample, said spacer region sequence being chosen from any of the sequences as represented by SEQ ID NO 76 to 106, 157 to 174, 124, 125, 111 to 115, 139 to 144, or 126 to 130, and with said probes or equivalents being possibly used in combination with any probe detecting at least one of the following organisms: Haemophilus influenzae, Streptococcus pneumoniae, Moraxella catarrhalis or Bordetella pertussis.

3. Method according to claim 1, wherein said sample is a sample taken from the cerebrospinal fluid, and wherein the set of probes as described in step (iii) comprises at least

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one probe chosen from the following spacer probes:

MYC-ICG-1 :	ACTGGATAGTGGTTGCGAGCATCTA	(SEQ ID NO 1)
MYC-ICG-22 :	CTTCTGAATAGTGGTTGCGAGCATCT	(SEQ ID NO 2)
MTB-ICG-1 :	GGGTGCATGACAACAAAGTTGGCCA	(SEQ ID NO 3)
MTB-ICG-2 :	GACTTGTTCCAGGTGTTGTCCCAC	(SEQ ID NO 4)
MTB-ICG-3 :	CGGCTAGCGGTGGCGTGTTCT	(SEQ ID NO 5)
LIS-ICG 1 :	CAAGTAACCGAGAATCATCTGAAAGTGAATC	(SEQ ID NO 39)
LMO-ICG 1 :	AAACAACCTTTACTTCGTAGAAGTAAATTGGTTAAG	(SEQ ID NO 40)
LMO-ICG 2 :	TGAGAGGTTAGTACTTCTCAGTATGTTTGTTC	(SEQ ID NO 41)
LMO-ICG 3 :	AGGCACTATGCTTGAAGCATCGC	(SEQ ID NO 42)
LISP-ICG 1:	CGTTTTCATAAGCGATCGCACGTT	(SEQ ID NO 212)

and preferably from the following spacer probes:

MYC-ICG-1 :	ACTGGATAGTGGTTGCGAGCATCTA	(SEQ ID NO 1)
MYC-ICG-22 :	CTTCTGAATAGTGGTTGCGAGCATCT	(SEQ ID NO 2)
MTB-ICG-1 :	GGGTGCATGACAACAAAGTTGGCCA	(SEQ ID NO 3)
MTB-ICG-2 :	GACTTGTTCCAGGTGTTGTCCCAC	(SEQ ID NO 4)
MTB-ICG-3 :	CGGCTAGCGGTGGCGTGTTCT	(SEQ ID NO 5)
LIS-ICG 1 :	CAAGTAACCGAGAATCATCTGAAAGTGAATC	(SEQ ID NO 39)
LMO-ICG 3 :	AGGCACTATGCTTGAAGCATCGC	(SEQ ID NO 42)
LISP-ICG 1:	CGTTTTCATAAGCGATCGCACGTT	(SEQ ID NO 212)

or equivalents of said probes,

and/or wherein the set of probes comprises at least one taxon-specific probe derived from the spacer region sequence corresponding to one of the micro-organisms to be detected in said sample, said spacer region sequence being chosen from any of the sequences as represented by SEQ ID NO 116, 118-121, or 213-215,

and with said probes or equivalents being possibly used in combination with any probe detecting at least one of the following organisms: Neisseria meningitidis, Haemophilus influenzae or Streptococcus pneumoniae.

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4. Method according to claim 1, wherein said sample is originating from the uro-genital tract, and wherein the set of probes as described in step (iii) comprises at least one probe chosen from the following spacer probes:

CHTR-ICG 1 : GGAAGAAGCCTGAGAAGGTTTCTGAC (SEQ ID NO 45)
CHTR-ICG 2 : GCATTTATATGTAAGAGCAAGCATTCTATTTCA (SEQ ID NO 46)
CHTR-ICG 3 : GAGTAGCGTGGTGAGGACGAGA (SEQ ID NO 47)
CHTR-ICG 4 : GAGTAGCGCGGTGAGGACGAGA (SEQ ID NO 201)
CHPS-ICG 1 : GGATAACTGTCTTAGGACGGTTTGAC (SEQ ID NO 48)
MGE-ICG 1 : CACCCATTAATTTTTTCGGTGTTAAAACCC (SEQ ID NO 51)
Mycoplasma-ICG : CAAAACTGAAAACGACAATCTTTCTAGTTCC (SEQ ID NO 52)

or equivalents of said probes,

and/or wherein the set of probes comprises at least one taxon-specific probe derived from the spacer region sequence corresponding to one of the micro-organisms to be detected in said sample, said spacer region sequence being chosen from any of the sequences as represented by SEQ ID NO 122, 123, 197, 124 or 125,

with said probes or equivalents being possibly used in combination with any probe detecting at least one of the following organisms: Neisseria gonorrhoeae, Haemophilus ducrevi or Streptococcus agalactiae.

5. Method according to claim 1, wherein said sample is originating from food, and wherein the set of probes as defined in step (iii) comprises at least one probe chosen from the following spacer probes:

LIS-ICG 1 : CAAGTAACCGAGAATCATCTGAAAGTGAATC (SEQ ID NO 39)
LMO-ICG 1 : AAACAACCTTTACTTCGTAGAAGTAAATTGGTTAAG (SEQ ID NO 40)
LMO-ICG 2 : TGAGAGGTTAGTACTTCTCAGTATGTTTGTTC (SEQ ID NO 41)
LMO-ICG 3 : AGGCACTATGCTTGAAGCATCGC (SEQ ID NO 42)
LIV-ICG 1 : GTTAGCATAAATAGGTAACTATTTATGACACAAGTAAC (SEQ ID NO 43)
LSE-ICG 1 :AGTTAGCATAAGTAGTGTAACTATTTATGACACAAG (SEQ ID NO 44)
LISP-ICG 1: CGTTTTCATAAGCGATCGCACGTT (SEQ ID NO 212)
STAU-ICG 1 : TACCAAGCAAAACCGAGTGAATAAAGAGTT (SEQ ID NO 53)

STAU-ICG 2 :	CAGAAGATGCGGAATAACGTGAC	(SEQ ID NO 54)
STAU-ICG 3 :	AACGAAGCCGTATGTGAGCATTTGAC	(SEQ ID NO 55)
STAU-ICG 4 :	GAACGTAACTTCATGTTAACGTTTGACTTAT	(SEQ ID NO 56)
BRU-ICG 1 :	CGTGCCGCCTTCGTTTCTCTTT	(SEQ ID NO 59)
BRU-ICG 2 :	TTCGCTTCGGGGTGGATCTGTG	(SEQ ID NO 60)
BRU-ICG 3 :	GCGTAGTAGCGTTTGCGTCGG	(SEQ ID NO 193)
BRU-ICG 4 :	CGCAAGAAGCTTGCTCAAGCC	(SEQ ID NO 194)
SALM-ICG 1 :	CAAAACTGACTTACGAGTCACGTTTGAG	(SEQ ID NO 61)
SALM-ICG 2 :	GATGTATGCTTCGTTATTCCACGCC	(SEQ ID NO 62)
STY-ICG 1 :	GGTCAAACCTCCAGGGACGCC	(SEQ ID NO 63)
SED-ICG 1 :	GCGGTAATGTGTGAAAGCGTTGCC	(SEQ ID NO 64)
YEC-ICG 1 :	GGAAAAGGTACTGCACGTGACTG	(SEQ ID NO 198)
YEC-ICG 2 :	GACAGCTGAAACTTATCCCTCCG	(SEQ ID NO 199)
YEC-ICG 3 :	GCTACCTGTTGATGTAATGAGTCAC	(SEQ ID NO 200)

and preferably from the following spacer probes:

LIS-ICG 1 :	CAAGTAACCGAGAATCATCTGAAAGTGAATC	(SEQ ID NO 39)
LMO-ICG 3 :	AGGCACTATGCTTGAAGCATCGC	(SEQ ID NO 42)
LISP-ICG 1:	CGTTTTCATAAGCGATCGCACGTT	(SEQ ID NO 212)
STAU-ICG 1 :	TACCAAGCAAAACCGAGTGAATAAAGAGTT	(SEQ ID NO 53)
STAU-ICG 2 :	CAGAAGATGCGGAATAACGTGAC	(SEQ ID NO 54)
STAU-ICG 3 :	AACGAAGCCGTATGTGAGCATTTGAC	(SEQ ID NO 55)
STAU-ICG 4 :	GAACGTAACTTCATGTTAACGTTTGACTTAT	(SEQ ID NO 56)
BRU-ICG 2 :	TTCGCTTCGGGGTGGATCTGTG	(SEQ ID NO 60)
BRU-ICG 3 :	GCGTAGTAGCGTTTGCGTCGG	(SEQ ID NO 193)
BRU-ICG 4 :	CGCAAGAAGCTTGCTCAAGCC	(SEQ ID NO 194)
SALM-ICG 1 :	CAAAACTGACTTACGAGTCACGTTTGAG	(SEQ ID NO 61)
YEC-ICG 1 :	GGAAAAGGTACTGCACGTGACTG	(SEQ ID NO 198)
YEC-ICG 2 :	GACAGCTGAAACTTATCCCTCCG	(SEQ ID NO 199)
YEC-ICG 3 :	GCTACCTGTTGATGTAATGAGTCAC	(SEQ ID NO 200)

or equivalents of said probes,

and/or wherein the set of probes comprises at least one taxon-specific probe derived from the spacer region sequence corresponding to one of the micro-organisms to be detected in said

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sample, said spacer region sequence being chosen from any of the sequences as represented by SEQ ID NO 116, 118-121, 213-215, 139-144, 131, 132, 154, 133-138, 195 or 196, with said probes or equivalents being possibly used in combination with any probe detecting strains of Campylobacter species.

6. Method according to claim 1, wherein said sample is originating from the gastro-intestinal tract of a patient, and wherein the set of probes as defined in step (iii) comprises at least one probe chosen from the following spacer probes:

SALM-ICG 1 :	CAAAACTGACTTACGAGTCACGTTTGAG	(SEQ ID NO 61)
SALM-ICG 2 :	GATGTATGCTTCGTTATTCCACGCC	(SEQ ID NO 62)
STY-ICG 1 :	GGTCAAACCTCCAGGGACGCC	(SEQ ID NO 63)
SED-ICG 1 :	GCGGTAATGTGTGAAAGCGTTGCC	(SEQ ID NO 64)
YEC-ICG 1 :	GGAAAAGGTACTGCACGTGACTG	(SEQ ID NO 198)
YEC-ICG 2 :	GACAGCTGAAACTTATCCCTCCG	(SEQ ID NO 199)
YEC-ICG 3 :	GCTACCTGTTGATGTAATGAGTCAC	(SEQ ID NO 200)

and preferably from the following spacer probes:

SALM-ICG 1 :	CAAAACTGACTTACGAGTCACGTTTGAG	(SEQ ID NO 61)
YEC-ICG 1 :	GGAAAAGGTACTGCACGTGACTG	(SEQ ID NO 198)
YEC-ICG 2 :	GACAGCTGAAACTTATCCCTCCG	(SEQ ID NO 199)
YEC-ICG 3 :	GCTACCTGTTGATGTAATGAGTCAC	(SEQ ID NO 200)

or equivalents of said probes,

and/or wherein the set of probes comprises at least one taxon-specific probe derived from the spacer region sequence corresponding to one of the micro-organisms to be detected in said sample, said spacer region sequence being chosen from any of the sequences as represented by SEQ ID NO 133-138 or 195-196,

with said probes or equivalents being possibly used in combination with any probe detecting Campylobacter species.

7. Method according to claim 1 to detect and identify one or more strains of Mycobacterium species and subspecies in a sample, wherein step (iii) comprises hybridizing to at least one of the following probes:

MYC-ICG-1 :	ACTGGATAGTGGTTGCGAGCATCTA	(SEQ ID NO 1)

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MYC-ICG-22 :	CTTCTGAATAGTGGTTGCGAGCATCT	(SEQ ID NO 2)
MTB-ICG-1 :	GGGTGCATGACAACAAAGTTGGCCA	(SEQ ID NO 3)
MTB-ICG-2 :	GACTTGTTCCAGGTGTTGTCCCAC	(SEQ ID NO 4)
MTB-ICG-3 :	CGGCTAGCGGTGGCGTGTTCT	(SEQ ID NO 5)
MAI-ICG-1 :	CAACAGCAAATGATTGCCAGACACAC	(SEQ ID NO 6)
MIL-ICG-11 :	GAGGGGTTCCCGTCTGTAGTG	(SEQ ID NO 7)
MIL-ICG-22 :	TGAGGGGTTCTCGTCTGTAGTG	(SEQ ID NO 8)
MAC-ICG-1 :	CACTCGGTCGATCCGTGTGGA	(SEQ ID NO 9)
MAV-ICG-1 :	TCGGTCCGTCCGTGTGGAGTC	(SEQ ID NO 10)
MAV-ICG-22 :	GTGGCCGGCGTTCATCGAAA	(SEQ ID NO 11)
MIN-ICG-1 :	GCATAGTCCTTAGGGCTGATGCGTT	(SEQ ID NO 12)
MIN-ICG-2 :	GCTGATGCGTTCGTCGAAATGTGTA	(SEQ ID NO 13)
MIN-ICG-22 :	CTGATGCGTTCGTCGAAATGTGT	(SEQ ID NO 14)
MIN-ICG-222 :	TGATGCGTTCGTCGAAATGTGT	(SEQ ID NO 15)
MIN-ICG-2222 :	GGCTGATGCGTTCGTCGAAATGTGTAA	(SEQ ID NO 16)
MAL-ICG-1 :	ACTAGATGAACGCGTAGTCCTTGT	(SEQ ID NO 17)
MHEF-ICG-1 :	TGGACGAAAACCGGGTGCACAA	(SEQ ID NO 18)
MAH-ICG-1 :	GTGTAATTTCTTTTTAACTCTTGTGTGTAAGTAAGTG	(SEQ ID NO 19)
MCO-ICG-11 :	TGGCCGGCGTGTTCATCGAAA	(SEQ ID NO 20)
MTH-ICG-11 :	GCACTTCAATTGGTGAAGTGCGAGCC	(SEQ ID NO 21)
MTH-ICG-2 :	GCGTGGTCTTCATGGCCGG	(SEQ ID NO 22)
MEF-ICG-11 :	ACGCGTGGTCCTTCGTGG	(SEQ ID NO 23)
MSC-ICG-1 :	TCGGCTCGTTCTGAGTGGTGTC	(SEQ ID NO 24)
MKA-ICG-1 :	GATGCGTTTGCTACGGGTAGCGT	(SEQ ID NO 25)
MKA-ICG-2 :	GATGCGTTGCCTACGGGTAGCGT	(SEQ ID NO 26)
MKA-ICG-3 :	ATGCGTTGCCCTACGGGTAGCGT	(SEQ ID NO 27)
MKA-ICG-4 :	CGGGCTCTGTTCGAGAGTTGTC	(SEQ ID NO 28)
MKA-ICG-5 :	CCCTCAGGGATTTTCTGGGTGTTG	(SEQ ID NO 182)
MKA-ICG-6 :	GGACTCGTCCAAGAGTGTTGTCC	(SEQ ID NO 183)
MKA-ICG-7 :	TCGGGCTTGGCCAGAGCTGTT	(SEQ ID NO 184)
MKA-ICG-8 :	GGGTGCGCAACAGCAAGCGA	(SEQ ID NO 185)

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MKA-ICG-9 :	GATGCGTTGCCCCTACGGG	(SEQ ID NO 186)
MKA-ICG-10 :	CCCTACGGGTAGCGTGTTCTTTTG	(SEQ ID NO 187)
MCH-ICG-1 :	GGTGTGGACTTTGACTTCTGAATAG	(SEQ ID NO 29)
MCH-ICG-2 :	CGGCAAAACGTCGGACTGTCA	(SEQ ID NO 30)
MGO-ICG-1 :	AACACCCTCGGGTGCTGTCC	(SEQ ID NO 31)
MGO-ICG-2 :	GTATGCGTTGTCGTTCGCGGC	(SEQ ID NO 32)
MGO-ICG-5 :	CGTGAGGGGTCATCGTCTGTAG	(SEQ ID NO 33)
MUL-ICG-1 :	GGTTTCGGGATGTTGTCCCACC	(SEQ ID NO 175)
MGV-ICG-1 :	CGACTGAGGTCGACGTGGTGT	(SEQ ID NO 176)
MGV-ICG-2 :	GGTGTTTGAGCATTGAATAGTGGTTGC	(SEQ ID NO 177)
MXE-ICG-1 :	GTTGGGCAGCAGGCAGTAACC	(SEQ ID NO 178)
MSI-ICG-1 :	CCGGCAACGGTTACGTGTTC	(SEQ ID NO 179)
MFO-ICG-1 :	TCGTTGGATGGCCTCGCACCT	(SEQ ID NO 180)
MFO-ICG-2 :	ACTTGGCGTGGGATGCGGGAA	(SEQ ID NO 181)
MML-ICG-1 :	CGGATCGATTGAGTGCTTGTCCC	(SEQ ID NO 188)
MML-ICG-2 :	TCTAAATGAACGCACTGCCGATGG	(SEQ ID NO 189)
MCE-ICG-1 :	TGAGGGAGCCCGTGCCTGTA	(SEQ ID NO 190)
MHP-ICG-1 :	CATGTTGGGCTTGATCGGGTGC	(SEQ ID NO 191)

and more preferably to at least one probe of the following restricted group of spacer probes:

MYC-ICG-1 :	ACTGGATAGTGGTTGCGAGCATCTA	(SEQ ID NO 1)
MYC-ICG-22 :	CTTCTGAATAGTGGTTGCGAGCATCT	(SEQ ID NO 2)
MTB-ICG-1 :	GGGTGCATGACAACAAAGTTGGCCA	(SEQ ID NO 3)
MTB-ICG-2 :	GACTTGTTCCAGGTGTTGTCCCAC	(SEQ ID NO 4)
MTB-ICG-3 :	CGGCTAGCGGTGGCGTGTTCT	(SEQ ID NO 5)
MAI-ICG-1 :	CAACAGCAAATGATTGCCAGACACAC	(SEQ ID NO 6)
MIL-ICG-11 :	GAGGGGTTCCCGTCTGTAGTG	(SEQ ID NO 7)
MIL-ICG-22 :	TGAGGGGTTCTCGTCTGTAGTG	(SEQ ID NO 8)
MAC-ICG-1 :	CACTCGGTCGATCCGTGTGGA	(SEQ ID NO 9)
MAV-ICG-1 :	TCGGTCCGTCCGTGTGGAGTC	(SEQ ID NO 10)
MAV-ICG-22 :	GTGGCCGGCGTTCATCGAAA	(SEQ ID NO 11)
MIN-ICG-1 :	GCATAGTCCTTAGGGCTGATGCGTT	(SEQ ID NO 12)
MAL-ICG-1 :	ACTAGATGAACGCGTAGTCCTTGT	(SEQ ID NO 17)

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MCO-ICG-11 :	TGGCCGGCGTGTTCATCGAAA	(SEQ ID NO 20)
MTH-ICG-11 :	GCACTTCAATTGGTGAAGTGCGAGCC	(SEQ ID NO 21)
MTH-ICG-2 :	GCGTGGTCTTCATGGCCGG	(SEQ ID NO 22)
MEF-ICG-11 :	ACGCGTGGTCCTTCGTGG	(SEQ ID NO 23)
MSC-ICG-1 :	TCGGCTCGTTCTGAGTGGTGTC	(SEQ ID NO 24)
MKA-ICG-3 :	ATGCGTTGCCCTACGGGTAGCGT	(SEQ ID NO 27)
MKA-ICG-4 :	CGGGCTCTGTTCGAGAGTTGTC	(SEQ ID NO 28)
MKA-ICG-5 :	CCCTCAGGGATTTTCTGGGTGTTG	(SEQ ID NO 182)
MKA-ICG-6 :	GGACTCGTCCAAGAGTGTTGTCC	(SEQ ID NO 183)
MKA-ICG-7 :	TCGGGCTTGGCCAGAGCTGTT	(SEQ ID NO 184)
MKA-ICG-8 :	GGGTGCGCAACAGCAAGCGA	(SEQ ID NO 185)
MKA-ICG-9 :	GATGCGTTGCCCCTACGGG	(SEQ ID NO 186)
MKA-ICG-10 :	CCCTACGGGTAGCGTGTTCTTTTG	(SEQ ID NO 187)
MCH-ICG-1 :	GGTGTGGACTTTGACTTCTGAATAG	(SEQ ID NO 29)
MCH-ICG-2 :	CGGCAAAACGTCGGACTGTCA	(SEQ ID NO 30)
MCH-ICG-3 :	GGTGTGGTCCTTGACTTATGGATAG	(SEQ ID NO 210)
MGO-ICG-5 :	CGTGAGGGGTCATCGTCTGTAG	(SEQ ID NO 33)
MUL-ICG-1 :	GGTTTCGGGATGTTGTCCGACC	(SEQ ID NO 175)
MGV-ICG-1 :	CGACTGAGGTCGACGTGGTGT	(SEQ ID NO 176)
MGV-ICG-2 :	GGTGTTTGAGCATTGAATAGTGGTTGC	(SEQ ID NO 177)
MGV-ICG-3 :	TCGGGCCGCGTGTTCGTCAAA	(SEQ ID NO 211)
MXE-ICG-1 :	GTTGGGCAGCAGGCAGTAACC	(SEQ ID NO 178)
MSI-ICG-1 :	CCGGCAACGGTTACGTGTTC	(SEQ ID NO 179)
MFO-ICG-1 :	TCGTTGGATGGCCTCGCACCT	(SEQ ID NO 180)
MFO-ICG-2 :	ACTTGGCGTGGGATGCGGGAA	(SEQ ID NO 181)
MML-ICG-1 :	CGGATCGATTGAGTGCTTGTCCC	(SEQ ID NO 188)
MML-ICG-2 :	TCTAAATGAACGCACTGCCGATGG	(SEQ ID NO 189)
MCE-ICG-1 :	TGAGGGAGCCCGTGCCTGTA	(SEQ ID NO 190)
MHP-ICG-1 :	CATGTTGGGCTTGATCGGGTGC	(SEQ ID NO 191)

or to equivalents of said probes,

and/or to any probe derived from SEQ ID NO 76-110, or 157-174 provided said probe hybridizes specifically to a Mycobacterium species.

8. Method according to claim 7, to detect and identify one or more Mycobacterium tuberculosis complex strains in a sample, wherein step (iii) comprises hybridizing to at least one of the following probes:

MTB-ICG-1 : GGGTGCATGACAACAAAGTTGGCCA (SEQ ID NO 3)
MTB-ICG-2 : GACTTGTTCCAGGTGTTGTCCCAC (SEQ ID NO 4)
MTB-ICG-3 : CGGCTAGCGGTGGCGTGTTCT (SEQ ID NO 5)

or to equivalents of said probes,
and/or to any probe derived from SEQ ID NO 76 provided said probe hybridizes specifically to the M. tuberculosis complex.

9. Method according to claim 7 to detect and identify one or more Mycobacterium strains from the MAIS-complex, wherein step (iii) comprises hybridizing to at least one of the following probes:

MAI-ICG-1 : CAACAGCAAATGATTGCCAGACACAC (SEQ ID NO 6)
MIL-ICG-11 : GAGGGGTTCCCGTCTGTAGTG (SEQ ID NO 7)
MIL-ICG-22 : TGAGGGGTTCTCGTCTGTAGTG (SEQ ID NO 8)
MAC-ICG-1 : CACTCGGTCGATCCGTGTGGA (SEQ ID NO 9)
MAV-ICG-1 : TCGGTCCGTCCGTGTGGAGTC (SEQ ID NO 10)
MAV-ICG-22 : GTGGCCGGCGTTCATCGAAA (SEQ ID NO 11)
MIN-ICG-1 : GCATAGTCCTTAGGGCTGATGCGTT (SEQ ID NO 12)
MIN-ICG-2 : GCTGATGCGTTCGTCGAAATGTGTA (SEQ ID NO 13)
MIN-ICG-22 : CTGATGCGTTCGTCGAAATGTGT (SEQ ID NO 14)
MIN-ICG-222 : TGATGCGTTCGTCGAAATGTGT (SEQ ID NO 15)
MIN-ICG-2222 : GGCTGATGCGTTCGTCGAAATGTGTAA (SEQ ID NO 16)
MAL-ICG-1 : ACTAGATGAACGCGTAGTCCTTGT (SEQ ID NO 17)
MHEF-ICG-1 : TGGACGAAAACCGGGTGCACAA (SEQ ID NO 18)
MAH-ICG-1 : GTGTAATTTCTTTTTTAACTCTTGTGTGTAAGTAAGTG (SEQ ID NO 19)
MCO-ICG-11 : TGGCCGGCGTGTTCATCGAAA (SEQ ID NO 20)
MTH-ICG-11 : GCACTTCAATTGGTGAAGTGCGAGCC (SEQ ID NO 21)
MTH-ICG-2 : GCGTGGTCTTCATGGCCGG (SEQ ID NO 22)

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MEF-ICG-11 : ACGCGTGGTCCTTCGTGG (SEQ ID NO 23)

MSC-ICG-1 : TCGGCTCGTTCTGAGTGGTGTC (SEQ ID NO 24)

or to equivalents of said probes,

and/or to any probe derived from SEQ ID NO 77-100 or 108-110, provided said probe hybridizes specifically to strains from the MAIS complex.

10. Method according to claim 9 to detect and identify one or more M. avium and M. paratuberculosis strains in a sample, wherein step (iii) comprises hybridizing to at least one of the following probes:

MAV-ICG-1 : TCGGTCCGTCCGTGTGGAGTC (SEQ ID NO 10)

MAV-ICG-22 : GTGGCCGGCGTTCATCGAAA (SEQ ID NO 11)

or to equivalents of said probes,

and/or to any probe derived from SEQ ID NO 77 and 78 provided said probe hybridizes specifically to M. avium or M. paratuberculosis.

11. Method according to claim 9 to detect and identify one or more Mycobacterium intracellulare strains and MIC-strains in a sample, wherein step (iii) comprises hybridizing to at least one of the following probes:

MAI-ICG-1 : CAACAGCAAATGATTGCCAGACACAC (SEQ ID NO 6)

MIL-ICG-11 : GAGGGGTTCCCGTCTGTAGTG (SEQ ID NO 7)

MIL-ICG-22 : TGAGGGGTTCTCGTCTGTAGTG (SEQ ID NO 8)

MAC-ICG-1 : CACTCGGTCGATCCGTGTGGA (SEQ ID NO 9)

MIN-ICG-1 : GCATAGTCCTTAGGGCTGATGCGTT (SEQ ID NO 12)

MIN-ICG-2 : GCTGATGCGTTCGTCGAAATGTGTA (SEQ ID NO 13)

MIN-ICG-22 : CTGATGCGTTCGTCGAAATGTGT (SEQ ID NO 14)

MIN-ICG-222 : TGATGCGTTCGTCGAAATGTGT (SEQ ID NO 15)

MIN-ICG-2222 : GGCTGATGCGTTCGTCGAAATGTGTAA (SEQ ID NO 16)

MAL-ICG-1 : ACTAGATGAACGCGTAGTCCTTGT (SEQ ID NO 17)

MHEF-ICG-1 : TGGACGAAAACCGGGTGCACAA (SEQ ID NO 18)

MAH-ICG-1 : GTGTAATTTCTTTTTTAACTCTTGTGTGTAAGTAAGTG (SEQ ID NO 19)

MCO-ICG-11 : TGGCCGGCGTGTTCATCGAAA (SEQ ID NO 20)

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MTH-ICG-11 : GCACTTCAATTGGTGAAGTGCGAGCC (SEQ ID NO 21)
MTH-ICG-2 : GCGTGGTCTTCATGGCCGG (SEQ ID NO 22)
MEF-ICG-11 : ACGCGTGGTCCTTCGTGG (SEQ ID NO 23),
or to equivalents of said probes,
and/or to any probe derived from SEQ ID NO 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98 or 99 provided said probe hybridizes specifically to M. intracellulare strains and MIC-strains.

12. Method according to claim 9 to detect and identify one or more Mycobacterium intracellulare strains in a sample, wherein step (iii) comprises hybrdizing to the following probe:
MIN-ICG-1 : GCATAGTCCTTAGGGCTGATGCGTT (SEQ ID NO 12),
or to equivalents of said probe,
and/or to any probe derived from SEQ ID NO 89 provided said probe hybridizes specifically to M. intracellulare.

13. Method according to claim 9 to detect and identify one or more Mycobacterium scrofulaceum strains in a sample, wherein step (iii) comprises hybrdizing to the following probe:
MSC-ICG-1 : TCGGCTCGTTCTGAGTGGTGTC (SEQ ID NO 24),
or to equivalents of said probe,
and/or to any probe derived from SEQ ID NO 100 provided said probe hybridizes specifically to M. scrofulaceum.

14. Method according to claim 7 to detect and identify one or more Mycobacterium kansasii strains in a sample, wherein step (iii) comprises hybridizing to at least one of the following probes:
MKA-ICG-1 : GATGCGTTTGCTACGGGTAGCGT (SEQ ID NO 25)
MKA-ICG-2 : GATGCGTTGCCTACGGGTAGCGT (SEQ ID NO 26)
MKA-ICG-3 : ATGCGTTGCCCTACGGGTAGCGT (SEQ ID NO 27)
MKA-ICG-4 : CGGGCTCTGTTCGAGAGTTGTC (SEQ ID NO 28)
MKA-ICG-5 : CCCTCAGGGATTTTCTGGGTGTTG (SEQ ID NO 182)

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MKA-ICG-6 : GGACTCGTCCAAGAGTGTTGTCC (SEQ ID NO 183)
MKA-ICG-7 : TCGGGCTTGGCCAGAGCTGTT (SEQ ID NO 184)
MKA-ICG-8 : GGGTGCGCAACAGCAAGCGA (SEQ ID NO 185)
MKA-ICG-9 : GATGCGTTGCCCCTACGGG (SEQ ID NO 186)
MKA-ICG-10 : CCCTACGGGTAGCGTGTTCTTTTG (SEQ ID NO 187)

and more preferably to:

MKA-ICG-3 : ATGCGTTGCCCTACGGGTAGCGT (SEQ ID NO 27)
MKA-ICG-4 : CGGGCTCTGTTCGAGAGTTGTC (SEQ ID NO 28),
MKA-ICG-5 : CCCTCAGGGATTTTCTGGGTGTTG (SEQ ID NO 182)
MKA-ICG-6 : GGACTCGTCCAAGAGTGTTGTCC (SEQ ID NO 183)
MKA-ICG-7 : TCGGGCTTGGCCAGAGCTGTT (SEQ ID NO 184)
MKA-ICG-8 : GGGTGCGCAACAGCAAGCGA (SEQ ID NO 185)
MKA-ICG-9 : GATGCGTTGCCCCTACGGG (SEQ ID NO 186)
MKA-ICG-10 : CCCTACGGGTAGCGTGTTCTTTTG (SEQ ID NO 187)

or to equivalents of said probes,
and/or to any probe derived from SEQ ID NO 101, 167, 168, or 169 provided said probe hybridizes specifically to M. kansasii.

15. Method according to claim 7 to detect and identify one or more Mycobacterium chelonae strains in a sample, wherein step (iii) comprises hybridizing to at least one of the following probes:

MCH-ICG-1 : GGTGTGGACTTTGACTTCTGAATAG (SEQ ID NO 29)
MCH-ICG-2 : CGGCAAAACGTCGGACTGTCA (SEQ ID NO 30)
MCH-ICG-3 : GGTGTGGTCCTTGACTTATGGATAG (SEQ ID NO 210)

or to equivalents of said probes,
and/or to any probe derived from SEQ ID NO 102, 103 or 174 provided said probe hybridizes specifically to M. chelonae.

16. Method according to claim 7 to detect and identify one or more Mycobacterium gordonae strains in a sample, wherein step (iii) comprises hybridizing to at least one of the following probes:

MGO-ICG-1 : AACACCCTCGGGTGCTGTCC (SEQ ID NO 31)

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MGO-ICG-2 : GTATGCGTTGTCGTTCGCGGC (SEQ ID NO 32)

MGO-ICG-5 : CGTGAGGGGTCATCGTCTGTAG (SEQ ID NO 33)

and more preferably to:

MGO-ICG-5 : CGTGAGGGGTCATCGTCTGTAG (SEQ ID NO 33),

or to equivalents of said probes,

and/or to any probe derived from SEQ ID NO 104, 105 or 106 provided said probe hybridizes specifically to M. gordonae.

17. Method according to claim 7 to detect and identify one or more Mycobacterium ulcerans strains or M. marinum strains in a sample, wherein step (iii) comprises hybridizing to the following probe:

MUL-ICG-1 : GGTTTCGGGATGTTGTCCCACC (SEQ ID NO 175)

or to equivalents of said probe,

and/or to any probe derived from SEQ ID NO 157 provided said probe hybridizes specifically to M. ulcerans and M. marinum.

18. Method according to claim 7 to detect and identify one or more Mycobacterium genavense strains in a sample, wherein step (iii) comprises hybridizing to the following probe:

MGV-ICG-1 : CGACTGAGGTCGACGTGGTGT (SEQ ID NO 176)

MGV-ICG-2 : GGTGTTTGAGCATTGAATAGTGGTTGC (SEQ ID NO 177)

MGV-ICG-3 : TCGGGCCGCGTGTTCGTCAAA (SEQ ID NO 211)

or to equivalents of said probes,

and/or to any probe derived from SEQ ID NO 158, 159, 160, 161 or 162 provided said probe hybridizes specifically to M. genavense.

19. Method according to claim 7 to detect and identify one or more Mycobacterium xenopi strains in a sample, wherein step (iii) comprises hybridizing to the following probe:

MXE-ICG-1 : GTTGGGCAGCAGGCAGTAACC (SEQ ID NO 178)

or to equivalents of said probe,

and/or to any probe derived from SEQ ID NO 163, provided said probe hybridizes specifically to M. xenopi.

20. Method according to claim 7 to detect and identify one or more Mycobacterium simiae strains in a sample, wherein step (iii) comprises hybridizing to the following probe:
MSI-ICG-1 : CCGGCAACGGTTACGTGTTC (SEQ ID NO 179)
or to equivalents of said probe,
and/or to any probe derived from SEQ ID NO 164 or 165 provided said probe hybridizes specifically to M. simiae.

21. Method according to claim 7 to detect and identify one or more Mycobacterium fortuitum strains in a sample, wherein step (iii) comprises hybridizing to the following probe:
MFO-ICG-1 : TCGTTGGATGGCCTCGCACCT (SEQ ID NO 180)
MFO-ICG-2 : ACTTGGCGTGGGATGCGGGAA (SEQ ID NO 181)
or to equivalents of said probes,
and/or to any probe derived from SEQ ID NO 166, provided said probe hybridizes specifically to M. fortuitum.

22. Method according to claim 7 to detect and identify one or more Mycobacterium celatum strains in a sample, wherein step (iii) comprises hybridizing to the following probe:
MCE-ICG-1 : TGAGGGAGCCCGTGCCTGTA (SEQ ID NO 190)
or to equivalents of said probe,
and/or to any probe derived from SEQ ID NO 170, provided said probe hybridizes specifically to M. celatum.

23. Method according to claim 7 to detect and identify one or more Mycobacterium haemophilum strains in a sample, wherein step (iii) comprises hybridizing to the following probe:
MHP-ICG-1 : CATGTTGGGCTTGATCGGGTGC (SEQ ID NO 191)
or to equivalents of said probe,
and/or to any probe derived from SEQ ID NO 171, 172 or 173, provided said probe hybridizes specifically to M. haemophilum.

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24. Method according to claim 7 to detect and identify one or more Mycobacterium strains in a sample, wherein step (iii) comprises hybridizing to at least one of the following probes:

MYC-ICG-1 : ACTGGATAGTGGTTGCGAGCATCTA (SEQ ID NO 1)

MYC-ICG-22 : CTTCTGAATAGTGGTTGCGAGCATCT (SEQ ID NO 2)

or to equivalents of said probes.

25. Method according to claim 1 to detect and identify one or more Mycoplasma strains in a sample, wherein step (iii) comprises hybridizing to at least one of the following probes:

MPN-ICG 1 : ATCGGTGGTAAATTAAACCCAAATCCCTGT (SEQ ID NO 49)

MPN-ICG 2 : CAGTTCTGAAAGAACATTTCCGCTTCTTTC (SEQ ID NO 50)

MGE-ICG 1 : CACCCATTAATTTTTTCGGTGTTAAAACCC (SEQ ID NO 51)

Mycoplasma-ICG : CAAAACTGAAAACGACAATCTTTCTAGTTCC (SEQ ID NO 52)

or to equivalents of said probes,

and/or to any probe derived from SEQ ID NO 124 or 125 provided said probe hybridizes specifically with Mycoplasma species.

26. Method according to claim 25 to detect and identify one or more Mycoplasma pneumoniae strains in a sample, wherein step (iii) comprises hybridizing to at least one of the following probes:

MPN-ICG 1 : ATCGGTGGTAAATTAAACCCAAATCCCTGT (SEQ ID NO 49)

MPN-ICG 2 : CAGTTCTGAAAGAACATTTCCGCTTCTTTC (SEQ ID NO 50)

or to equivalents of said probes,

and/or to any probe derived from SEQ ID NO 125 provided said probe hybridizes specifically to Mycoplasma pneumoniae.

27. Method according to claim 25 to detect and identify one or more Mycoplasma genitalium strains in a sample, wherein step (iii) comprises hybridizing to the following probe:

MGE-ICG 1 : CACCCATTAATTTTTTCGGTGTTAAAACCC (SEQ ID NO 51)

or to equivalents of said probe,

or to any probe derived from SEQ ID NO 124 provided said probe hybridizes specifically to Mycoplasma genitalium.

28. Method according to claim 1 to detect and identify one or more Pseudomonas strains in a sample, wherein step (iii) comprises hybridizing to at least one of the following probes:

PA-ICG 1 : TGGTGTGCTGCGTGATCCGAT (SEQ ID NO 34)

PA-ICG 2 : TGAATGTTCGTGGATGAACATTGATT (SEQ ID NO 35)

PA-ICG 3 : CACTGGTGATCATTCAAGTCAAG (SEQ ID NO 36)

PA-ICG 4 : TGAATGTTCGT(G/A)(G/A)ATGAACATTGATTTCTGGTC (SEQ ID NO 37)

PA-ICG 5 : CTCTTTCACTGGTGATCATTCAAGTCAAG (SEQ ID NO 38),

or to equivalents of said probes,

and/or to any probe derived from SEQ ID NO 111, 112, 113, 114 or 115 provided said probe hybridizes specifically to Pseudomonas strains.

29. Method according to claim 28 to detect and identify one or more Pseudomonas aeruginosa strains in a sample, wherein step (iii) comprises hybridizing to at least one of the following probes:

PA-ICG 1 : TGGTGTGCTGCGTGATCCGAT (SEQ ID NO 34)

PA-ICG 2 : TGAATGTTCGTGGATGAACATTGATT (SEQ ID NO 35)

PA-ICG 3 : CACTGGTGATCATTCAAGTCAAG (SEQ ID NO 36)

PA-ICG 4 : TGAATGTTCGT(G/A)(G/A)ATGAACATTGATTTCTGGTC (SEQ ID NO 37)

PA-ICG 5 : CTCTTTCACTGGTGATCATTCAAGTCAAG (SEQ ID NO 38),

and most preferably to at least one of the following probes:

PA-ICG 1 : TGGTGTGCTGCGTGATCCGAT (SEQ ID NO 34)

PA-ICG 4 : TGAATGTTCGT(G/A)(G/A)ATGAACATTGATTTCTGGTC (SEQ ID NO 37)

PA-ICG 5 : CTCTTTCACTGGTGATCATTCAAGTCAAG (SEQ ID NO 38)

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or to equivalents of said probes,
and/or to any probe derived from SEQ ID NO 111 provided said probe hybridizes specifically to Pseudomonas aeruginosa.

30. Method according to claim 1 to detect and identify one or more Staphylococcus species in a sample, wherein step (iii) comprises hybridizing to at least one of the following probes:

STAU-ICG 1 : TACCAAGCAAAACCGAGTGAATAAAGAGTT (SEQ ID NO 53)
STAU-ICG 2 : CAGAAGATGCGGAATAACGTGAC (SEQ ID NO 54)
STAU-ICG 3 : AACGAAGCCGTATGTGAGCATTTGAC (SEQ ID NO 55)
STAU-ICG 4 : GAACGTAACTTCATGTTAACGTTTGACTTAT (SEQ ID NO 56)

or to equivalents of said probes,
and/or to any probe derived from SEQ ID NO 139, 140, 141, 142 ,143 or 144 provided said probe hybridizes specifically to Staphylococcus species.

31. Method according to claim 30 to detect and identify one or more Staphylococcus aureus strains, wherein step (iii) comprises hybridizing to at least one, and preferably both of the following probes:

STAU-ICG 3 : AACGAAGCCGTATGTGAGCATTTGAC (SEQ ID NO 55)
STAU-ICG 4 : GAACGTAACTTCATGTTAACGTTTGACTTAT (SEQ ID NO 56).

or to equivalents of said probes,
and/or to any probe derived from SEQ ID NO 139, 140, 141, 142 or 143 provided said probe hybridizes specifically to Staphylococcus aureus.

32. Method according to claim 30 to detect and identify one or more Staphylococcus epidermidis strains in a sample, wherein step (iii) comprises hybridizing to any probe derived from SEQ ID NO 144 provided said probe hybridizes specifically to Staphylococcus epidermidis.

33. Method according to claim 1 to detect and identify one or more Acinetobacter strains in a sample, wherein step (iii) comprises hybridizing to at least one of the following probes:

ACI-ICG 1 : GCTTAAGTGCACAGTGCTCTAAACTGA (SEQ ID NO 57)
ACI-ICG 2 : CACGGTAATTAGTGTGATCTGACGAAG (SEQ ID NO 58),
or to equivalents of said probes,
and/or to any probe derived from SEQ ID NO 126, 127, 128, 129 or 130 provided said probe hybridizes specifically to Acinetobacter sp..

34. Method according to claim 33 to detect and identify one or more Acinetobacter baumanii strains in a sample, wherein step (iii) comprises hybridizing to at least one of the ollowing probes:
ACI-ICG 1 : GCTTAAGTGCACAGTGCTCTAAACTGA (SEQ ID NO 57)
ACI-ICG 2 : CACGGTAATTAGTGTGATCTGACGAAG (SEQ ID NO 58)
or to equivalents of said probes,
and/or to any probe derived from SEQ ID NO 126 provided said probe hybridizes specifically to Acinetobacter baumanii.

35. Method according to claim 1 to detect and identify one or more Listeria strains in a sample, wherein step (iii) comprises hybridizing to at least one of the following probes:
LIS-ICG 1 : CAAGTAACCGAGAATCATCTGAAAGTGAATC (SEQ ID NO 39)
LMO-ICG 1 : AAACAACCTTTACTTCGTAGAAGTAAATTGGTTAAG
(SEQ ID NO 40)
LMO-ICG 2 : TGAGAGGTTAGTACTTCTCAGTATGTTTGTTC (SEQ ID NO 41)
LMO-ICG 3 : AGGCACTATGCTTGAAGCATCGC (SEQ ID NO 42)
LIV-ICG 1 : GTTAGCATAAATAGGTAACTATTTATGACACAAGTAAC
(SEQ ID NO 43)
LSE-ICG 1 : AGTTAGCATAAGTAGTGTAACTATTTATGACACAAG
LISP-ICG 1: CGTTTTCATAAGCGATCGCACGTT (SEQ ID NO 212)
and most preferably to at least one of the following probes:
LIS-ICG 1 : CAAGTAACCGAGAATCATCTGAAAGTGAATC (SEQ ID NO 39)
LMO-ICG 3 : AGGCACTATGCTTGAAGCATCGC (SEQ ID NO 42)
LISP-ICG 1: CGTTTTCATAAGCGATCGCACGTT (SEQ ID NO 212)
or to equivalents of said probes,

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and/or to any probe derived from SEQ ID NO 116, 118, 119, 120, 121, 213, 214 or 215 provided said probe hybridizes specifically to Listeria species.

36. Method according to claim 35 to detect and identify one or more Listeria monocytogenes strains in a sample, wherein step (iii) comprises hybridizing to at least one of the following probes:

LMO-ICG 1 : AAACAACCTTTACTTCGTAGAAGTAAATTGGTTAAG (SEQ ID NO 40)

LMO-ICG 2 : TGAGAGGTTAGTACTTCTCAGTATGTTTGTTC (SEQ ID NO 41)

LMO-ICG 3 : AGGCACTATGCTTGAAGCATCGC (SEQ ID NO 42)

and most preferably to the following probe:

LMO-ICG 3 : AGGCACTATGCTTGAAGCATCGC (SEQ ID NO 42)

or to equivalents of said probes,

and/or to any probe derived from SEQ ID NO 118 or 120 provided said probe hybridizes specifically to Listeria monocytogenes.

37. Method according to claim 1 to detect and identify one or more Brucella strains in a sample, wherein step (iii) comprises hybridizing to at least one of the following probes:

BRU-ICG 1 : CGTGCCGCCTTCGTTTCTCTTT (SEQ ID NO 59)

BRU-ICG 2 : TTCGCTTCGGGGTGGATCTGTG (SEQ ID NO 60)

BRU-ICG 3 : GCGTAGTAGCGTTTGCGTCGG (SEQ ID NO 193)

BRU-ICG 4 : CGCAAGAAGCTTGCTCAAGCC (SEQ ID NO 194)

and most preferably to the following probe:

BRU-ICG 2 : TTCGCTTCGGGGTGGATCTGTG (SEQ ID NO 60)

BRU-ICG 3 : GCGTAGTAGCGTTTGCGTCGG (SEQ ID NO 193)

BRU-ICG 4 : CGCAAGAAGCTTGCTCAAGCC (SEQ ID NO 194)

or to equivalents of said probes,

and/or to any probe derived from SEQ ID NO 131, 132 or 154 provided said probe hybridizes specifically to Brucella strains.

38. Method according to claim 1 to detect and identify one or more Salmonella strains

in a sample, wherein step (iii) comprises hybridizing to at least one of the following probes:

SALM-ICG 1 : CAAAACTGACTTACGAGTCACGTTTGAG (SEQ ID NO 61)
SALM-ICG 2 : GATGTATGCTTCGTTATTCCACGCC (SEQ ID NO 62)
STY-ICG 1 : GGTCAAACCTCCAGGGACGCC (SEQ ID NO 63)
SED-ICG 1 : GCGGTAATGTGTGAAAGCGTTGCC (SEQ ID NO 64)

and most preferably to the following probe:

SALM-ICG 1 : CAAAACTGACTTACGAGTCACGTTTGAG (SEQ ID NO 61)

or to equivalents of said probes,
and/or to any probe derived from SEQ ID NO 133, 134, 135, 136, 137 or 138 provided said probe hybridizes specifically to Salmonella strains.

39. Method according to claim 1 to detect and identify one or more Chlamydia strains in a sample, wherein step (iii) comprises hybridizing to at least one of the following probes:

CHTR-ICG 1 : GGAAGAAGCCTGAGAAGGTTTCTGAC (SEQ ID NO 45)
CHTR-ICG 2 : GCATTTATATGTAAGAGCAAGCATTCTATTTCA (SEQ ID NO 46)
CHTR-ICG 3 : GAGTAGCGTGGTGAGGACGAGA (SEQ ID NO 47)
CHTR-ICG 4 : GAGTAGCGCGGTGAGGACGAGA (SEQ ID NO 201)
CHPS-ICG 1 : GGATAACTGTCTTAGGACGGTTTGAC (SEQ ID NO 48)

or to equivalents of said probes,
and/or to any probe derived from SEQ ID NO 122, 123 or 197 provided that said probe hybridizes specifically to Chlamydia strains.

40. Method according to claim 39 to detect and identify one or more Chlamydia trachomatis strains in a sample, wherein step (iii) comprises hybridizing to at least one of the following probes:

CHTR-ICG 1 : GGAAGAAGCCTGAGAAGGTTTCTGAC (SEQ ID NO 45)
CHTR-ICG 2 : GCATTTATATGTAAGAGCAAGCATTCTATTTCA (SEQ ID NO 46)
CHTR-ICG 3 : GAGTAGCGTGGTGAGGACGAGA (SEQ ID NO 47)
CHTR-ICG 4 : GAGTAGCGCGGTGAGGACGAGA (SEQ ID NO 201)

or to equivalents of said probes,

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and/or to any probe derived from SEQ ID NO 123 or 197 provided said probe hybridizes specifically to Chlamydia trachomatis.

41. Method according to claim 39 to detect and identify one or more Chlamydia psittaci strains in a sample, wherein step (iii) comprises hybridizing to at least the following probe:

CHPS-ICG 1 : GGATAACTGTCTTAGGACGGTTTGAC (SEQ ID NO 48)

or to equivalents of said probe,

and/or to any probe derived from SEQ ID NO 122 provided said probe hybridizes specifically to Chlamydia psittaci.

42. Method according to claim 1 to detect one or more Streptococcus strains in a sample, wherein step (iii) comprises hybridizing to any probe derived from SEQ ID NO 145, 146, 147, 148, 149, 150, 151, 152 or 153 provided said probe hybridizes specifically to Streptococcus strains.

43. Method according to claim 1, to detect and identify specifically Chlamydia trachomatis in a sample, wherein step (ii) comprises amplification of the 16S-23S rRNA spacer region or a part of it, using at least one of the following primers:

CHTR-P1: AAGGTTTCTGACTAGGTTGGGC (SEQ ID NO 69)

CHTR-P2: GGTGAAGTGCTTGCATGGATCT (SEQ ID NO 70)

or equivalents of these primers, said equivalents differing in sequence from the above mentioned primers by changing one or more nucleotides, provided that said equivalents still amplify specifically the spacer region or part of it of Chlamydia trachomatis.

44. Method according to claim 1, to detect and identify specifically Listeria species in a sample, wherein step (ii) comprises amplification of the 16S-23S rRNA spacer region or a part of it, using at least one of the following primers:

LIS-P1 : ACCTGTGAGTTTTCGTTCTTCTC (SEQ ID NO 71)

LIS-P2 : CTATTTGTTCAGTTTTGAGAGGTT (SEQ ID NO 72)

LIS-P3 : ATTTTCCGTATCAGCGATGATAC (SEQ ID NO 73)

LIS-P4 : ACGAAGTAAAGGTTGTTTTTCT (SEQ ID NO 74)
LIS-P5 : GAGAGGTTACTCTCTTTTATGTCAG (SEQ ID NO 75)
LIS-P6 : CTTTTATGTCAGATAAAGTATGCAA (SEQ ID NO 202)
LIS-P7 : CGTAAAAGGGTATGATTATTTG (SEQ ID NO 203)

or equivalents of these primers, said equivalents differing in sequence from the above mentioned primers by changing one or more nucleotides, provided that said equivalents still amplify specifically the spacer region or part of it of Listeria species.

45. Method according to claim 1, to detect and identify specifically Mycobacterium species in a sample, wherein step (ii) comprises amplification of the 16S-23S rRNA spacer region or a part of it, using at least one of the following primers:

MYC-P1: TCCCTTGTGGCCTGTGTG (SEQ ID NO 65)
MYC-P2: TCCTTCATCGGCTCTCGA (SEQ ID NO 66)
MYC-P3: GATGCCAAGGCATCCACC (SEQ ID NO 67)
MYC-P4: CCTCCCACGTCCTTCATCG (SEQ ID NO 68)
MYC-P5: CCTGGGTTTGACATGCACAG (SEQ ID NO 192)

or equivalents of these primers, said equivalents differing in sequence from the above mentioned primers by changing one or more nucleotides, provided that said equivalents still amplify specifically the spacer region or part of it of Mycobacterium species.

46. Composition comprising at least one of the probes or primers as defined in claims 1 to 45 and 51 to 53.

47. Probe as defined in any of claims 1 to 42 and 51.

48. Primer as defined in any of claims 43 to 45 and 52 to 53.

49. Reverse hybridization method comprising any of the probes as defined in claims 1 to 42 and 51 wherein said probes are immobilized on a known location on a solid support, more preferably on a membrane strip.

50. Kit for the detection and identification of at least one micro-organism, or the

simultaneous detection and identification of several micro-organisms in a sample, comprising the following components:

(i) when appropiate, at least one suitable primer pair to allow amplification of the 16S-23S rRNA spacer region, or a part of it;

(ii) at least one of the probes as defined in claims 1 to 42 and 51;

(iii) a buffer, or components necessary to produce the buffer, enabling a hybridization reaction between said probes and the polynucleic acids present in the sample, or the amplified products thereof;

(iv) a solution, or components necessary for producing the solution, enabling washing of the hybrids formed under the appropiate wash conditions;

(v) when appropiate, a means for detecting the hybrids resulting from the preceding hybridization.

51. Method according to claim 1 to detect and identify one or more Yersinia enterocolitica strains in a sample, wherein step (iii) comprises hybridizing to at least one of the following probes :

YEC-ICG 1 : GGAAAAGGTACTGCACGTGACTG (SEQ ID NO 198)
YEC-ICG 2 : GACAGCTGAAACTTATCCCTCCG (SEQ ID NO 199)
YEC-ICG 3 : GCTACCTGTTGATGTAATGAGTCAC (SEQ ID NO 200)

or to equivalents of said probes,
and/or to any probe derived from SEQ ID NO 195 or 196, provided said probe hybridizes specifically to Yersinia enterocolitica strains.

52. Method according to claim 1, to detect and identify specifically Brucella species in a sample, wherein step (ii) comprises amplification of the 16S-23S rRNA spacer region or a part of it, using at least one of the following primers :

BRU-P1 : TCGAGAATTGGAAAGAGGTC (SEQ ID NO 204)
BRU-P2 : AAGAGGTCGGATTTATCCG (SEQ ID NO 205)
BRU-P3 : TTCGACTGCAAATGCTCG (SEQ ID NO 206)
BRU-P4 : TCTTAAAGCCGCATTATGC (SEQ ID NO 207)

or equivalents of these primers, said equivalents differing in sequence from the above mentioned primers by changing one or more nucleotides, provided that said equivalents still

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amplify specifically the spacer region or part of it of Brucella species.

53. Method according to claim 1, to detect and identify specifically Yersinia enterocolitica species in a sample, wherein step (ii) comprises amplification of the 16S-23S rRNA spacer region or a part of it, using at least one of the following primers :

YEC-P1 : CCTAATGATATTGATTCGCG (SEQ ID NO 208)

YEC-P2 : ATGACAGGTTAATCCTTACCCC (SEQ ID NO 209)

or equivalents of these primers, said equivalents differing in sequence from the above mentioned primers by changing one or more nucleotides, provided that said equivalents still amplify specifically the spacer region or part of it of Yersinia enterocolitica species.

Add A17

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